

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Lal, Preeti  
Corley, Neil C.  
Shah, Purvi
- (ii) TITLE OF THE INVENTION: HUMAN RETICULOCALBIN ISOFORMS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Hereewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0358 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-855-0555
  - (B) TELEFAX: 650-845-4166
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 328 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: RATRNOT02
  - (B) CLONE: 922578

Met 1	Met	Trp	Arg	Pro 5	Ser	Val	Leu	Leu	Leu 10	Leu	Leu	Leu	Leu	Arg 15	His
Gly	Ala	Gln	Gly 20	Lys	Pro	Ser	Pro	Asp 25	Ala	Gly	Pro	His	Gly 30	Gln	Gly
Arg	Val	His 35	Gln	Ala	Ala	Pro	Leu 40	Ser	Asp	Ala	Pro	His 45	Asp	Asp	Ala
His	Gly 50	Asn	Phe	Gln	Tyr	Asp 55	His	Glu	Ala	Phe	Leu 60	Gly	Arg	Glu	Val
Ala 65	Lys	Glu	Phe	Asp 70	Gln	Leu	Thr	Pro	Glu	Glu 75	Ser	Gln	Ala	Arg	Leu 80
Gly	Arg	Ile	Val	Asp 85	Arg	Met	Asp	Arg	Ala 90	Gly	Asp	Gly	Asp	Gly 95	Trp
Val	Ser	Leu	Ala 100	Glu	Leu	Arg	Ala	Trp 105	Ile	Ala	His	Thr	Gln 110	Gln	Arg
His	Ile 115	Arg	Asp	Ser	Val	Ser	Ala 120	Ala	Trp	Asp	Thr	Tyr 125	Asp	Thr	Asp
Arg	Asp 130	Gly	Arg	Val	Gly	Trp 135	Glu	Glu	Leu	Arg	Asn 140	Ala	Thr	Tyr	Gly
His 145	Tyr	Ala	Pro	Gly 150	Glu	Phe	His	Asp	Val 155	Glu	Asp	Ala	Glu	Thr 160	
Tyr	Lys	Lys	Met 165	Leu	Ala	Arg	Asp	Glu 170	Arg	Arg	Phe	Arg	Val 175	Ala	Asp
Gln	Asp	Gly	Asp 180	Ser	Met	Ala	Thr	Arg 185	Glu	Glu	Leu	Thr 190	Ala	Phe	Leu
His	Pro 195	Glu	Glu	Phe	Pro	His	Met 200	Arg	Asp	Ile	Val 205	Ile	Ala	Glu	Thr
Leu	Glu 210	Asp	Leu	Asp	Arg	Asn 215	Lys	Asp	Gly	Tyr	Val 220	Gln	Val	Glu	Glu
Tyr 225	Ile	Ala	Asp	Leu 230	Tyr	Ser	Ala	Glu	Pro	Gly 235	Glu	Glu	Glu	Pro	Ala
Trp	Val	Gln	Thr 245	Glu	Arg	Gln	Gln	Phe	Arg 250	Asp	Phe	Arg	Asp	Leu 255	Asn
Lys	Asp	Gly	His 260	Leu	Asp	Gly	Ser	Glu 265	Val	Gly	His	Trp 270	Val	Leu	Pro
Pro	Ala	Gln	Asp 275	Gln	Pro	Leu	Val 280	Glu	Ala	Asn	His 285	Leu	Leu	His	Glu
Ser	Asp 290	Thr	Asp	Lys	Asp	Gly 295	Arg	Leu	Ser	Lys	Ala 300	Glu	Ile	Leu	Gly
Asn 305	Trp	Asn	Met 310	Phe	Val	Gly	Ser	Gln	Ala	Thr 315	Asn	Tyr	Gly	Glu	Asp 320
Leu	Thr	Arg	His 325	His	Asp	Glu	Leu								

(A) LENGTH: 1463 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) LIBRARY: RATRNOT02  
(B) CLONE: 922578

CGCAGAGCGG ACGTGGAGAG CGGACGNCAG CTGGATAACA GGGGACCGAT GATGTGGCGA 60  
CCATCAGTTC TGCTGCTTCT GTTGCTACTG AGGCACGGGG CCCAGGGGAA GCCATCCCCA 120

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GACGCAGGCC CTCATGGCCA GGGGAGGGTG CACCAGGCGG CCCCCCTGAG CGACGCTCCC 180
CATGATGACG CCCACGGGAA CTTCCAGTAC GACCATGAGG CTTTCCTGGG ACGGGAAGTG 240
GCCAAGGAAT TCGACCAACT CACCCCAGAG GAAAGCCAGG CCCGTCTGGG GCGGATCGTG 300
GACCGCATGG ACCGCGCGGG GGACGGCGAC GGCTGGGTGT CGCTGGCCGA GCTTCGCGCG 360
TGGATCGCGC ACACGCAGCA GCGGCACATA CGGGACTCGG TGAGCGCGGC CTGGGACACG 420
TACGACACGG ACCGCGACGG GCGTGTGGGT TGGGAGGAGC TGGCAACGC CACCTATGGC 480
CACTACGCGC CCGGTGAAGA ATTTTCATGAC GTGGAGGATG CAGAGACCTA CAAAAAGATG 540
CTGGCTCGGG ACGAGCGGCG TTTCCGGGTG GCCGACCAGG ATGGGGACTC GATGGCCACT 600
CGAGAGGAGC TGACAGCCTT CCTGCACCCC GAGGAGTTCC CTCACATGCG GGACATCGTG 660
ATTGCTGAAA CCTTGAGGGA CCTGGACAGA AACAAAGATG GCTATGTCCA GGTGGAGGAG 720
TACATCGCGG ATCTGTACTC AGCCGAGCCT GGGGAGGAGG AGCCGGCGTG GGTGCAGACG 780
GAGAGGCAGC AGTTCCGGGA CTTCCGGGAT CTGAACAAGG ATGGGCACCT GGATGGGAGT 840
GAGGTGGGCC ACTGGGTGCT GCCCCCTGCC CAGGACCAGC CCCTGGTGGA AGCCAACCAC 900
CTGCTGCACG AGAGCGACAC GGACAAGGAT GGGCGGCTGA GCAAAGCGGA AATCCTGGGT 960
AATTGGAACA TGTTTGTGGG CAGTCAGGCC ACCAACTATG GCGAGGACCT GACCCGGCAC 1020
CACGATGAGC TGTGAGCACC GCGCACCTGC CACAGCCTCA GAGGCCCGCA CAATGACCGG 1080
AGGAGGGGCC GCTGTGGTCT GGCCCCCTCC CTGTCCAGGC CCCGAGGAG GCAGATGCAG 1140
TCCCAGGCAT CCTCTGCCCC CTGGGCTCTC AGGGACCCCC TGGGTGGCT TCTGTCCCTG 1200
TCACACCCCC AACCCAGGG AGGGCTGTG ATAGTCCCAG AGGATAAGCA ATACCTATTT 1260
CTGACTGAGT CTCCCAGCCC AGACCCAGGG ACCCTTGGCC CCAAGCTCAG CTCTAAGAAC 1320
CGCCCCAACC CCTCCAGCTC CAAATCTGAG CCTCCACCAC ATAGACTGAA ACTCCCCTGG 1380
CCCCAGCCCT CTCCTGCCTG GCCTGGCCTG GGACACCTCC TCTCTGCCAG GAGGCAATAA 1440
AAGCCAGCGC CGGGAAAAAA AAA 1463

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03
- (B) CLONE: 1601793

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 1          5          10          15
Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
 20          25          30
Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp
 35          40          45
His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Thr Phe Asp Gln Leu
 50          55          60
Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
 65          70          75          80
Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys Asp Trp
 85          90          95
Ile Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln
100          105          110
Trp Lys Gly His Asp Leu Asn Glu Asp Gly Leu Val Ser Trp Glu Glu
115          120          125
Tyr Lys Asn Ala Thr Tyr Gly Tyr Val Leu Asp Asp Pro Asp Pro Asp
130          135          140
Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe
145          150          155          160
Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe
165          170          175

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Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val  
 180 185 190  
 Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile  
 195 200 205  
 Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr  
 210 215 220  
 Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe  
 225 230 235 240  
 Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Glu Thr Lys Asp  
 245 250 255  
 Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His  
 260 265 270  
 Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu  
 275 280 285  
 Glu Ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp  
 290 295 300  
 Phe Gly Glu Ala Leu Val Arg His Asp Glu Phe  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2658 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03  
 (B) CLONE: 1601793

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCCTTCCG	GTTGGGCGGT	GCTTGCGCGC	GTGAGCTGAG	CCGGTGGGTG	AGCGGCGGCC	60
ACGGCATCCT	GTGCTGTGGG	GGCTACGAGG	AAAGATCTAA	TTATCATGGA	CCTGCGACAG	120
TTTCTTATGT	GCCTGTCCCT	GTGCACAGCC	TTTGCCTTGA	GCAAACCCAC	AGAAAAGAAG	180
GACCGTGTAC	ATCATGAGCC	TCAGCTCAGT	GACAAGGTTT	ACAATGATGC	TCAGAGTTTT	240
GATTATGACC	ATGATGCCTT	CTTGGGTGCT	GAAGAAGCAA	AGACCTTTGA	TCAGCTGACA	300
CCAGAAGAGA	GCAAGGAAAG	GCTTGGAAAG	ATTGTAAGTA	AAATAGATGG	CGACAAGGAC	360
GGGTTTGTCA	CTGTGGATGA	GCTCAAAGAC	TGGATTAAAT	TTGCACAAAA	GCGCTGGATT	420
TACGAGGATG	TAGAGCGACA	GTGGAAGGGG	CATGACCTCA	ATGAGGACGG	CCTCGTTTCC	480
TGGGAGGAGT	ATAAAAATGC	CACCTACGGC	TACGTTTTAG	ATGATCCAGA	TCCTGATGAT	540
GGATTTAATC	ATAAACAGAT	GATGGTTAGA	GATGAGCGGA	GGTTTAAAT	GGCAGACAAG	600
GATGGAGACC	TCATTGCCAC	CAAGGAGGAG	TTACACAGCTT	TCCTGCACCC	TGAGGAGTAT	660
GACTACATGA	AAGATATAGT	AGTACAGGAA	ACAATGGAAG	ATATAGATAA	GAATGCTGAT	720
GGTTTCATTG	ATCTAGAAGA	GTATATTGGT	GACATGTACA	GCCATGATGG	GAATACTGAT	780
GAGCCAGAAT	GGGTAAAGAC	AGAGCGAGAG	CAGTTTGTTG	AGTTTCGGGA	TAAGAACCGT	840
GATGGGAAGA	TGGACAAGGA	AGAGACCAAA	GACTGGATCC	TTCCCTCAGA	CTATGATCAT	900
GCAGAGGCAG	AAGCCAGGCA	CCTGGTCTAT	GAATCAGACC	AAAACAAGGA	TGGCAAGCTT	960
ACCAAGGAGG	AGATCGTTGA	CAAGTATGAC	TTATTTGTTG	GCAGCCAGGC	CACAGATTTT	1020
GGGGAGGCCCT	TAGTACGGCA	TGATGAGTTC	TGAGCTACGG	AGGAACCCCTC	ATTTCTCTCA	1080
AAGTAATTTA	TTTTTACAGC	TTCTGGTTTC	ACATGAAATT	GTTTGCCTGA	CTGAGACTGT	1140
TACTACAAC	TTTTTAAGAC	ATGAAAAGGC	GTAATGAAAA	CCATCCCGTC	CCCATTCTCT	1200
CTCCTCTCTG	AGGGACTGGA	GGGAAGCCGT	GCTTCTGAGG	AACAACCTCTA	ATTAGTACAC	1260
TTGTGTTTGT	AGATTTACAC	TTGTATTAT	GTATTAAACAT	GGCGTGTTTA	TTTTTGTATT	1320
TTTCTCTGGT	TGGGAGTATG	ATATGAAGGA	TCAAGATCCT	CAACTCACAC	ATGTAGACAA	1380
ACATTAGCTC	TTTACTCTTT	CTCAACCCCT	TTTATGATTT	TAATAATTCT	CACTTAACCTA	1440
ATTTTGTAAG	CCTGAGATCA	ATAAGAAATG	TTCAAGGAGAG	AGGAAAGAAA	AAAAATATAT	1500
GCTCCACAAT	TTATATTTAG	AGAGAGAACA	CTTAGTCTTG	CCTGTCAAAA	AGTCCAACAT	1560
TTCATAGGTA	GTAGGGGCCA	CATATTACAT	TCAGTTGCTA	TAGGTCCAGC	AACTGAACCT	1620
GCCATTACCT	GGGCAAGGAA	AGATCCCTTT	GCTCTAGGAA	AGCTTGGCCC	AAATTGATTT	1680

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TCTTCTTTTTT CCCCCTGTAG GACTGACTGT TGGCTAATTT TGTCAAGCAC AGCTGTGGTG 1740
GGAAGAGTTA GGGCCAGTGT CTTGAAAATC AATCAAGTAG TGAATGTGAT CTCTTTGCAG 1800
AGCTATAGAT AGAAACAGCT GGAAACTAA AGGAAAAATA CAAATGTTTT CGGGGCATAC 1860
ATTTTTTTTTC TGGGTGTGCA TCTGTTGAAA TGCTCAAGAC TTAATTATTT GCCTTTTGAA 1920
ATCACTGTAA ATGCCCCCAT CCGGTTCCCTC TTCTTCCAG GTGTGCCAAG GAATTAATCT 1980
TGGTTTCACT ACAATTAAAA TTCACTCCTT TCCAATCATG TCATTGAAAG TGCCTTTAAC 2040
GAAAGAAATG GTCACCTGAAT GGAATTCTC TTAAGAAACC CTGAGATTAA AAAAAGACTA 2100
TTTGGATAAC TTATAGGAAA GCCTAGAACC TCCAGTAGA GTGGGGATTT TTTTCTTCTT 2160
CCCTTTCTCT TTTGGACAAT AGTTAAATTA GCAGTATTAG TTATGAGTTT GGTTGCAGTG 2220
TTCTTATCTT GTGGGCTGAT TTCCAAAAAC CACATGCTGC TGAATTTACC AGGGATCCTC 2280
ATACCTCACA ATGCAAACCA CTTACTACCA GGCCTTTTTC TGTGTCCACT GGAGAGCTTG 2340
AGCTCACACT CAAAGATCAG AGGACCTACA GAGAGGGCTC TTTGGTTTGA GGACCATGGC 2400
TTACCTTTCC TGCCTTTGAC CCATCACACC CCATTTCCCTC CTCTTTCCCT CTCCCCGCTG 2460
CCAAAAAAGGA AAAAAAGGA AACGTTTATC ATGAATCAAC AGGGTTTCAG TCCTTATCAA 2520
AGAGAGATGT GGAAAGAGCT AAAGAAACCA CCCTTTGTTT CCAACTCCAC TTTACCCATA 2580
TTTTATGCAA CACAAACACT GTCCTTTTGG GTCCCTTTCT TACAGATGGG ACCTCTTGAG 2640
GAAGGAATTA TCGTATTC 2658

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## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1262329

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ala Arg Gly Gly Arg Gly Arg Arg Leu Gly Leu Ala Leu Gly Leu
 1          5          10          15
Leu Leu Ala Leu Val Leu Ala Pro Arg Val Leu Arg Ala Lys Pro Thr
 20          25          30
Val Arg Lys Glu Arg Val Val Arg Pro Asp Ser Glu Leu Gly Glu Arg
 35          40          45
Pro Pro Glu Asp Asn Gln Ser Phe Gln Tyr Asp His Glu Ala Phe Leu
 50          55          60
Gly Lys Glu Asp Ser Lys Thr Phe Asp Gln Leu Thr Pro Asp Glu Ser
 65          70          75          80
Lys Glu Arg Leu Gly Lys Ile Val Asp Arg Ile Asp Asn Asp Gly Asp
 85          90          95
Gly Phe Val Thr Thr Glu Glu Leu Lys Thr Trp Ile Lys Arg Val Gln
100          105          110
Lys Arg Tyr Ile Phe Asp Asn Val Ala Lys Val Trp Lys Asp Tyr Asp
115          120          125
Arg Asp Lys Asp Asp Lys Ile Ser Trp Glu Glu Tyr Lys Gln Ala Thr
130          135          140
Tyr Gly Tyr Tyr Leu Gly Asn Pro Ala Glu Phe His Asp Ser Ser Asp
145          150          155          160
His His Thr Phe Lys Met Leu Pro Arg Asp Glu Arg Arg Phe Lys
165          170          175
Ala Ala Asp Leu Asn Gly Asp Leu Thr Ala Thr Arg Glu Glu Phe Thr
180          185          190
Ala Phe Leu His Pro Glu Glu Phe Glu His Met Lys Glu Ile Val Val
195          200          205
Leu Glu Thr Leu Glu Asp Ile Asp Lys Asn Gly Asp Gly Phe Val Asp
210          215          220

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PF-0358-2 DIV

Gln	Asp	Glu	Tyr	Ile	Ala	Asp	Met	Phe	Ser	His	Glu	Glu	Asn	Gly	Pro
225					230					235					240
Glu	Pro	Asp	Trp	Val	Leu	Ser	Glu	Arg	Glu	Gln	Phe	Asn	Glu	Phe	Arg
				245					250						255
Asp	Leu	Asn	Lys	Asp	Gly	Lys	Leu	Asp	Lys	Asp	Glu	Ile	Arg	His	Trp
		260						265						270	
Ile	Leu	Pro	Gln	Asp	Tyr	Asp	His	Ala	Gln	Ala	Glu	Ala	Arg	His	Leu
		275					280						285		
Val	Tyr	Glu	Ser	Asp	Lys	Asn	Lys	Asp	Glu	Lys	Leu	Thr	Lys	Glu	Glu
	290					295					300				
Ile	Leu	Glu	Asn	Trp	Asn	Met	Phe	Val	Gly	Ser	Gln	Ala	Thr	Asn	Tyr
305					310					315					320
Gly	Glu	Asp	Leu	Thr	Lys	Asn	His	Asp	Glu	Leu					
			325						330						

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

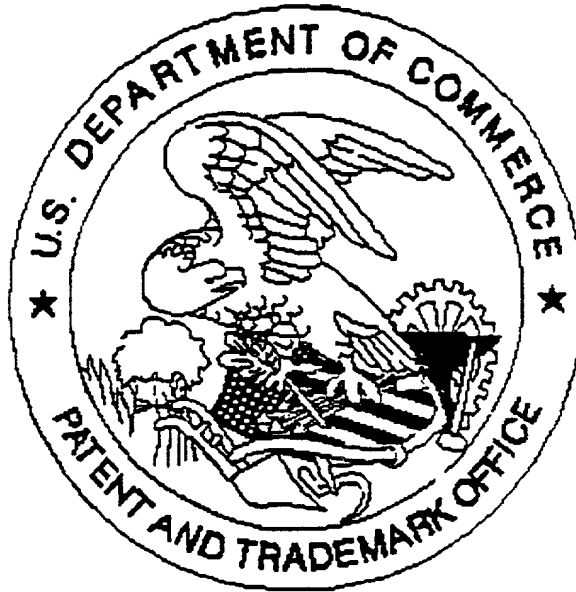
(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 780361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg	Arg	Asp	Val	Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser
1				5					10					15	
Gln	Ala	Arg	Leu	Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Leu	Ala	Gly	Asp
			20					25					30		
Ser	Asp	Gly	Trp	Val	Ser	Leu	Ala	Ala	Leu	Arg	Ala	Trp	Ile	Ala	His
		35					40					45			
Thr	Gln	Gln	Arg	His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	His	Thr
	50					55				60					
Tyr	Asp	Thr	Asp	Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn
65					70					75					80
Ala	Thr	Tyr	Gly	His	Tyr	Glu	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu
				85					90					95	
Gly	Pro														

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